

284 SerGluSerAlaLeuArgGlnArg-----GluTyr 294
1273 GGCTCTGCGGCTCACTGAGAGGCGATGAGATGATGCCAGAGCTTACCCAGGCC 1332
295 AlaGluLeuLeuArgGlyArgGlyLeuLeuArgSerLeuAlaLeuLeuSerAlaPhe 314
1333 TTCCGCTCTCTGCGAGACGAGAGGCGCGAGGCGCGATCGATCGAGAGCATCTT 1392
315 AlaLeuSerAlaPheProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
1393 GGCTCTGCGGCTCACTGAGAGGCGATGAGATGATGCCAGAGCTTACCCAGGCC 1452
335 GluArgProLeuSerValTyrTyrSerIleAlaPheThrLeuGlnTyrPheAsnSerPhe 354
1453 TCCGCTCTCTGCGAGACGAGAGGCGCGAGGCGCGATCGATCGAGAGCATCTT 1509
355 ValAsnProPheLeuTyrProLeuGlnIleArgArgPheGlnIleValAlaPheTyrValIle 374
1510 GTCAACCTCTGCTCTTACCTCTGCGACACAGCTTCCGCGGCTTACACAGCATG 1569
375 LeuGlyValIleTyr-----Tyr----- 380
1570 CTCTGCGGCGAGAGCTCAAAATCCAGGCCACAGCTCCGTGAGAGCATGCTGAAAGTA 1629
381 -----ProAlaLeuSerGlnAsnGlnSer 388
1630 GTGCGGCGAGAGCTCTCTGAGCGAGGCTCTCTGAGCGGCTT 1677

RESULT 4
US-08-985-090-1
Sequence 1, Application US/08985090
Patent No. 5,682,893
GENERAL INFORMATION:
APPLICANT: Andrew D. J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USBS THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSES: LAHIV & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
FEATURES:
NAME/KEY: CDS
LOCATION: 291..1625
US-08-985-090-1

Alignment Scores:
Pred. No.: 4,876-65 Length: 2689
Score: 724.50 Matches: 171
Percent Similarity: 48.90% Conservative: 52
Best Local Similarity: 37.50% Mismatches: 118
Query Match: 35.38% Indels: 115
DB: 2 Gaps: 12

US-10-626-445-8 (1-391) x US-08-985-090-1 (1-2689)

18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyValAlaValIle 37
399 CTGCGCGGCTCTGAGAGGCGATGAGATGATGCCAGAGCTTACCCAGGCC 458
38 LeuAlaPheValIleArgArgAlaLeuArgHISArgSerAlaTyrPhePheLeuAlaLeu 57
459 CTGCGCTCTGCGGCGAGCTGAGAGGCTGAGAGGCGAGAGGCGAGAGGCGAGAGG 518
58 AlaIleSerArgPheLeuValGlyLeuIleSerIleProLeuTyrIleProHISValLeu 77
519 GCATCTCCGAGCTCTCTGCGGCGCTTGCAGCTGAGAGGCGAGAGGCGAGAGGCGAG 578
78 Phe---AsnTyrAsnPheGlySerGlyIleCysMetPheTyrPheIleThrAspTyrLeu 96
579 ACAGCGGCTGAGAGCTTCCGCGGCGCTGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAG 638
97 LeuGlyThrAlaSerValTyrAsnIleValLeuIleSerTyrAsnArgTyrGlnSerVal 116
639 CTGTGACCTCTCTGAGAGGCGATGAGATGATGCCAGAGCTTACCCAGGCC 698
117 SerAlaAlaValSerTyrArgAlaGlnIleThrGlyIleMetValIleValAlaGlnMet 136
699 ACCGAGCGGCTCTGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAG 758
137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
759 CTCTGCTGTGAGGCTCTGAGAGGCGATGAGATGATGCCAGAGGCGAGAGGCGAGAGG 809
157 TyrIlePhe-----AsnSerThrAsnThrIleAspGlyGlnProGlyPheVal 171
810 TGGAGTACCTCTGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAG 869
172 ThrGluTyrTyrIleLeuThrIleThrMetIleLeuGlnPheLeuLeuProValIleSer 191
870 TAAACTGTACTCTCTGAGAGGCGATGAGATGATGCCAGAGGCGAGAGGCGAGAGGCGAG 929
192 ValAlaIleTyrPheAsnValGlnIleTyr----- 200
930 GTTACCTCTTTCATCTGAGAGGCGATGAGATGATGCCAGAGGCGAGAGGCGAGAGGCGAG 989
200 ----- 200
990 GATGCGGCTGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAG 1049
201 -----TyrSerLeuTyrPheArgAlaLeuSerArgGlyAspProSerHIS 215
1050 CACAGGCTGAGAGGCGATGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAG 1109
216 -----AlaGlyPheSerThrTyrSerSer 223
1110 AGTATGAGGCTGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAG 1169
224 SerAlaSerGlyHISLeuHISArgAlaGlyValAlaCysArgTyrSerAsnProGlyLeu 243
1170 GCGAGGCGAGGCG-----GCGCTGCTGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGGCG 1214
244 LybGluSerAlaAlaSerArgHISerGlySerProArgArgLybSerSerIleLeuVal 263
1215 -----AGCTCTCTGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAGAGGCGAG 1244
264 SerLeuArgThrHISMetAsnSerSerIleThrAlaPheLeuValGlySerPheThrArg 283

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Db      1245 -----TCACTCAAGAGGGCTTCAAGCCGTG 1271
Qy      284 SerGuseRAlaAlaLeuArgGlnArg-----GlnArg 294
Db      1272 GCGTCTCGGCTCACTGAGAGAGGCAATGCTGTCCAGAGCTTCAAGCCAGCC 1331
Qy      295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe 314
Db      1332 TTTCGGCTGTCTCGGAGACAGGAAAGTGGCAAGCTCCGCGCCCTCACTCGAGCACTCTT 1391
Qy      315 AlaIleCybTrpAlaProGlyArgGlyLeuPheThrIleValLeuSerThrArgProArgThr 334
Db      1392 GCGCTCTCTGCGGCGCCATACAGCTCTGTGATATATATCCGAGCGCCGCGCCAGCCAGC 1451
Qy      335 GlnArgProLeuSerValTyrTyrSerIleAlaPheTrpLeuGlnTrpPheAlaSerPhe 354
Db      1452 TGCCTCTCT--GACTACTGATACGAAACCTCTCTGCTCTCTGCGCCAACTCGGCT 1508
Qy      355 ValAlaProPheLeuTyrProLeuCybHlaArgArgPheGlnValAlaPheTrpValIle 374
Db      1509 GTCAACCTGTCTCTACCTCTGTGTGCACCAAGCTTCGCGCGGCTTCAAGCAAGCTG 1568
Qy      375 LeuCybValThrArg-----Trp-----380
Db      1569 CTGCGCCCAAGAGCTCAAAATTCAGCCCAAGCTCTCTGAGCACTCTGAGAGTGA 1628
Qy      381 -----ProAlaLeuSerGlnAlaGlnSer 388
Db      1629 GTGCGCCCAAGAGCTCTCTCTCAAGCCAGCTCTCTCAAGCCAGAGTCT 1676

RESULT 5
US-09-165-543-1
: Sequence 1, Application US/09165543
: Patent No. 6083545
: GENERAL INFORMATION:
: APPLICANT: Andrew D.J. Goodearl and Sandra Gluckeman
: TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
: NUMBER OF SEQUENCES: 39
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAMIVE & COCKFIELD, LLP
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/165,543
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/042,780
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Elizabeth A. Hanley
: REGISTRATION NUMBER: 33,505
: REFERENCE/DOCKET NUMBER: MNI-032CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)237-7400
: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2689 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FRATURE:
: NAME/KEY: CDS

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: LOCATION: 291..1625
US-09-165-543-1
Alignment Scores:
Pred. No.: 4,87e-65
Score: 724.50
Percent Similarity: 48.90%
Best Local Similarity: 37.50%
Query Match: 35.38%
DB: 3
Gaps: 12

US-10-626-445-8 (1-391) x US-09-165-543-1 (1-2689)
Qy      18 LeuAlaPheLeuMetSerSerPheAlaIleMetValGlyAlaAlaValValIle 37
Db      399 CTGGCGCGCTCATGCGCGCTGCTCATGCGCGCGCTGCGCGCGCGCGCGCGCGCGCG 458
Qy      38 LeuAlaPheValAlaPargAlaLeuArgHlaArgSerAlaArgPhePheLeuAlaLeu 57
Db      459 CTGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 518
Qy      58 AlaIleSerAlaPheLeuValGlyLeuIleSerIleProLeuTyrIleProHlaValLeu 77
Db      519 GCACTCTCGACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578
Qy      78 Phe--AenTrpAlaPheGlySerGlyIleCybMetPheTrpLeuIleThrApyTrpLeu 96
Db      579 ACAAGCGCGCTGACCTTCTGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 638
Qy      97 LeuCybThrAlaSerValTyrAlaAlaValIleLeuIleSerTyrAlaArgTyrAlaSerVal 116
Db      639 CTGTGCACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698
Qy      117 SerAlaAlaValAlaSerTyrAlaGlnAlaGlnIleThrGlyIleMetValIleAlaIleMet 136
Db      639 ACCGAGCGGTCTATACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 758
Qy      137 ValAlaValTyrIleLeuAlaPheLeuValAlaGlyIlePrometIleAlaAlaSerApySer 156
Db      759 CTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 809
Qy      157 TrpArg-----AenSerThrAenThrIleApyCybGluProGlyPheVal 171
Db      810 TGGGATGATCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 869
Qy      172 ThrGlnTyrTyrIleLeuThrIleThrMetLeuGlnPheLeuLeuProValIleSer 191
Db      870 TACAACCTGTCTCTCTCATACGCGCTTCCACCGCGCGCGCGCGCGCGCGCGCGCG 929
Qy      192 ValAlaTyrPheAlaValAlaGlnIleTyr-----200
Db      930 GTCACTCTTTTAACTTACACATCTTACGAAATTCAGAGCGGCGCGCGCGCGCGCG 989
Qy      200 -----200
Db      990 GATGGGCTCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1049
Qy      201 -----TrpSerLeuTyrTyrArgArgAlaLeuSerArgCybProSerHla 215
Db      1050 CCACCGCTGAGCTCTGTGGGCTGTGTGCGAGAGGCGCGCGCGCGCGCGCGCGCGCG 1109
Qy      216 -----AlaGlyPheSerThrThSerSer 223
Db      1110 AGGTATGGGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1169
Qy      224 SerAlaSerGlyHlaLeuHlaArgAlaGlyValAlaCybArgThrSerApyProGlyLeu 243
Db      1170 GCGCGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1214
Qy      244 LyGluSerAlaAlaSerArgHlaSerGluSerProArgArgGlySerSerIleLeuVal 263
Db      1215 -----AGCTCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1244

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